STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/583,110_

Source: _1 Fwp_

Date Processed by STIC: _6/27/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: _10/583,110_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
_____Wrapped Aminos was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
  prevent "wrapping."

2___✓___Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3_____Misaligned Amino The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
  Numbering use **space characters**, instead.

4_____Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
  ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
  each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
  residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
  "bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
  the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
  Artificial or Unknown sequences.**

7_____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
  (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
  (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
  This sequence is intentionally skipped
  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
  (NEW RULES) <210> sequence id number
  <400> sequence id number
  000

9_____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
  (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
  In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10_____Invalid <213> Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
  Response scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
  is Artificial Sequence. (see item 11 below)

11_____Use of <220> Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
  of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
  Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
  explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
  Sequence Rules

12_____PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
  "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
  listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFWP

```
RAW SEQUENCE LISTING              DATE: 06/27/2006
PATENT APPLICATION:  US/10/583,110    TIME: 11:56:31

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272006\J583110.raw
```

see Item 2 on Exec summary sheet

```
        2 <110> APPLICANT: Suntory Limited et al.
W-->    3 <120> TITLE OF INVENTION: Proess for production of yellow flowers by control of
flavonoid
W-->    4        synthesis system
W-->    5 <130> FILE REFERENCE: P952
C-->    6 <140> CURRENT APPLICATION NUMBER: US/10/583,110
C-->    6 <141> CURRENT FILING DATE: 2006-06-15
W-->    6 <160> NUMBER OF SEQ ID: 70
```

see pp 1, 3-12

ERRORED SEQUENCES

**Does Not Comply
Corrected Diskette Needed**

```
W-->    7 <210> SEQ ID NO: 1
        8 <211> LENGTH: 1422
        9 <212> TYPE: DNA
E-->   10 <213> ORGANISM:          <-- mandatory response needed
W-->   11 <220> FEATURE:
W-->   12 <221> NAME/KEY:
       13 <222> LOCATION:
       14 <223> OTHER INFORMATION: Nucleic acid in pSPB1725
W-->   15 <400> SEQUENCE: 1
       16 atg gga gaa gaa tac aag aaa aca cac aca ata gtc ttt cac act tca       48
       17 Met Gly Glu Glu Tyr Lys Lys Thr His Thr Ile Val Phe His Thr Ser
       18  1               5                  10                  15
       19 gaa gaa cac ctc aac tct tca ata gcc ctt gca aag ttc ata acc aaa       96
       20 Glu Glu His Leu Asn Ser Ser Ile Ala Leu Ala Lys Phe Ile Thr Lys
       21            20                  25                  30
       22 cac cac tct tca atc tcc atc act atc atc agc act gcc ccc gcc gaa      144
       23 His His Ser Ser Ile Ser Ile Thr Ile Ile Ser Thr Ala Pro Ala Glu
       24            35                  40                  45
       25 tct tct gaa gtg gcc aaa att att aat aat ccg tca ata act tac cgc      192
       26 Ser Ser Glu Val Ala Lys Ile Ile Asn Asn Pro Ser Ile Thr Tyr Arg
       27         50                  55                  60
       28 ggc ctc acc gcg gta gcg ctc cct gaa aat ctc acc agt aac att aat      240
       29 Gly Leu Thr Ala Val Ala Leu Pro Glu Asn Leu Thr Ser Asn Ile Asn
       30 65                  70                  75                  80
       31 aaa aac ccc gtc gaa ctt ttc ttc gaa atc cct cgt cta caa aac gcc      288
       32 Lys Asn Pro Val Glu Leu Phe Phe Glu Ile Pro Arg Leu Gln Asn Ala
       33                  85                  90                  95
       34 aac ctt cga gag gct tta cta gat att tcg cga aaa tcc gat atc aaa      336
       35 Asn Leu Arg Glu Ala Leu Leu Asp Ile Ser Arg Lys Ser Asp Ile Lys
       36             100                 105                 110
       37 gca tta atc atc gat ttc ttc tgc aat gcg gca ttt gaa gta tcc acc      384
       38 Ala Leu Ile Ile Asp Phe Phe Cys Asn Ala Ala Phe Glu Val Ser Thr
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: **US/10/583,110**   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
39              115                 120                    125
40 agc atg aac ata ccc act tac ttc gac gtc agt ggc ggc gct ttt ctc        432
41 Ser Met Asn Ile Pro Thr Tyr Phe Asp Val Ser Gly Gly Ala Phe Leu
42      130                 135                    140
43 ctc tgc acg ttt ctc cac cac ccg aca cta cac caa act gtt cgt gga        480
44 Leu Cys Thr Phe Leu His His Pro Thr Leu His Gln Thr Val Arg Gly
45 145                 150                    155                    160
46 gac att gcg gat ttg aac gat tct gtt gag atg ccc ggg ttc cca ttg        528
47 Asp Ile Ala Asp Leu Asn Asp Ser Val Glu Met Pro Gly Phe Pro Leu
48              165                 170                    175
49 att cac tcc tct gat tta cca atg agt ttg ttt tat cgt aag act aat        576
50 Ile His Ser Ser Asp Leu Pro Met Ser Leu Phe Tyr Arg Lys Thr Asn
51              180                 185                    190
52 gtt tac aaa cac ttt cta gac act tcc tta aac atg cgc aaa tcg agt        624
53 Val Tyr Lys His Phe Leu Asp Thr Ser Leu Asn Met Arg Lys Ser Ser
54      195                 200                    205
55 ggg ata ctc gtg aac acg ttt gtt gcg ctc gag ttt cga gct aag gaa        672
56 Gly Ile Leu Val Asn Thr Phe Val Ala Leu Glu Phe Arg Ala Lys Glu
57      210                 215                    220
58 gct ttg tcc aac ggt ttg tac ggt cca act ccg cct ctt tat tta ctt        720
59 Ala Leu Ser Asn Gly Leu Tyr Gly Pro Thr Pro Pro Leu Tyr Leu Leu
60 225                 230                    235                    240
61 tca cat aca att gcc gaa ccc cac gac act aaa gtg ttg gta aac caa        768
62 Ser His Thr Ile Ala Glu Pro His Asp Thr Lys Val Leu Val Asn Gln
63              245                 250                    255
64 cac gaa tgc cta tca tgg ctt gat ttg cag cct agt aaa agc gtg att        816
65 His Glu Cys Leu Ser Trp Leu Asp Leu Gln Pro Ser Lys Ser Val Ile
66              260                 265                    270
67 ttc ctt tgt ttc gga aga aga gga gcg ttc tca gca caa cag ttg aaa        864
68 Phe Leu Cys Phe Gly Arg Arg Gly Ala Phe Ser Ala Gln Gln Leu Lys´
69      275                 280                    285
70 gaa att gcg ata ggg ttg gag aag agt gga tgt cga ttt ctt tgg ttg        912
71 Glu Ile Ala Ile Gly Leu Glu Lys Ser Gly Cys Arg Phe Leu Trp Leu
72      290                 295                    300
73 gcc cgc att tca ccg gag atg gac tta aat gcg ctt ctg ccg gag ggt        960
74 Ala Arg Ile Ser Pro Glu Met Asp Leu Asn Ala Leu Leu Pro Glu Gly
75 305                 310                    315                    320
76 ttt cta tcg aga act aaa gga gta ggg ttt gtg aca aac aca tgg gtg       1008
77 Phe Leu Ser Arg Thr Lys Gly Val Gly Phe Val Thr Asn Thr Trp Val
78              325                 330                    335
79 ccg caa aaa gag gtg ttg agt cat gat gca gtg ggg ggg ttt gtg act       1056
80 Pro Gln Lys Glu Val Leu Ser His Asp Ala Val Gly Gly Phe Val Thr
81      340                 345                    350
82 cat tgc ggg tgg agt tcg gtt ctt gaa gcg ctg tcg ttc ggt gtc ccg       1104
83 His Cys Gly Trp Ser Ser Val Leu Glu Ala Leu Ser Phe Gly Val Pro
84      355                 360                    365
85 atg att ggt tgg ccg ttg tac gca gag cag agg atc aat agg gtg ttc       1152
86 Met Ile Gly Trp Pro Leu Tyr Ala Glu Gln Arg Ile Asn Arg Val Phe
87      370                 375                    380
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272006\J583110.raw

```
 88 atg gtg gag gaa ata aag gtg gcg ctg cca ttg gat gag gaa gat gga        1200
 89 Met Val Glu Glu Ile Lys Val Ala Leu Pro Leu Asp Glu Glu Asp Gly
 90 385                 390                 395                 400
 91 ttt gtg acg gcg atg gag ttg gag aag cgc gtc agg gag ttg atg gag        1248
 92 Phe Val Thr Ala Met Glu Leu Glu Lys Arg Val Arg Glu Leu Met Glu
 93                 405                 410                 415
 94 tcg gta aag ggg aaa gaa gtg aag cgc cgt gtg gcg gaa ttg aaa atc        1296
 95 Ser Val Lys Gly Lys Glu Val Lys Arg Arg Val Ala Glu Leu Lys Ile
 96                 420                 425                 430
 97 tct aca aag gca gcc gtg agt aaa ggt gga tcg tcc ttg gct tct ttg        1344
 98 Ser Thr Lys Ala Ala Val Ser Lys Gly Gly Ser Ser Leu Ala Ser Leu
 99                 435                 440                 445
100 gag aag ttc atc aac tcg gtc act cgt taaag tttcttactc aatatatggt        1396
101 Glu Lys Phe Ile Asn Ser Val Thr Arg
102         450                 455
103 acatcggttt aactaccaaa ttttat                                          1422
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 457
107 <212> TYPE: PRT
```

E--> 108 <213> ORGANISM: ←_mardatory response_ _insert the mardatory numeric identifier_

                                    <220> wherever <221>, <222>, or <223> is shown

```
109 <223> OTHER INFORMATION: Amino acid sequence of 4,2',4',6'-tetrahydroxychalcane 4'-O-
110         glycosyltransferase encoded in pSPB1725
```

@ --> 111 <400> SEQUENCE: 2

```
112 Met Gly Glu Glu Tyr Lys Lys Thr His Thr Ile Val Phe His Thr Ser
113   1                 5                  10                  15
114 Glu Glu His Leu Asn Ser Ser Ile Ala Leu Ala Lys Phe Ile Thr Lys
115                 20                  25                  30
116 His His Ser Ser Ile Ser Ile Thr Ile Ile Ser Thr Ala Pro Ala Glu
117                 35                  40                  45
118 Ser Ser Glu Val Ala Lys Ile Ile Asn Asn Pro Ser Ile Thr Tyr Arg
119         50                  55                  60
120 Gly Leu Thr Ala Val Ala Leu Pro Glu Asn Leu Thr Ser Asn Ile Asn
121  65                  70                  75                  80
122 Lys Asn Pro Val Glu Leu Phe Phe Glu Ile Pro Arg Leu Gln Asn Ala
123                 85                  90                  95
124 Asn Leu Arg Glu Ala Leu Leu Asp Ile Ser Arg Lys Ser Asp Ile Lys
125                 100                 105                 110
126 Ala Leu Ile Ile Asp Phe Phe Cys Asn Ala Ala Phe Glu Val Ser Thr
127         115                 120                 125
128 Ser Met Asn Ile Pro Thr Tyr Phe Asp Val Ser Gly Gly Ala Phe Leu
129     130                 135                 140
130 Leu Cys Thr Phe Leu His His Pro Thr Leu His Gln Thr Val Arg Gly
131 145                 150                 155                 160
132 Asp Ile Ala Asp Leu Asn Asp Ser Val Glu Met Pro Gly Phe Pro Leu
133         165                 170                 175
134 Ile His Ser Ser Asp Leu Pro Met Ser Leu Phe Tyr Arg Lys Thr Asn
135         180                 185                 190
136 Val Tyr Lys His Phe Leu Asp Thr Ser Leu Asn Met Arg Lys Ser Ser
137         195                 200                 205
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: **US/10/583,110**   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
138 Gly Ile Leu Val Asn Thr Phe Val Ala Leu Glu Phe Arg Ala Lys Glu
139     210                 215                 220
140 Ala Leu Ser Asn Gly Leu Tyr Gly Pro Thr Pro Pro Leu Tyr Leu Leu
141 225                 230                 235                 240
142 Ser His Thr Ile Ala Glu Pro His Asp Thr Lys Val Leu Val Asn Gln
143                 245                 250                 255
144 His Glu Cys Leu Ser Trp Leu Asp Leu Gln Pro Ser Lys Ser Val Ile
145                 260                 265                 270
146 Phe Leu Cys Phe Gly Arg Arg Gly Ala Phe Ser Ala Gln Gln Leu Lys
147             275                 280                 285
148 Glu Ile Ala Ile Gly Leu Glu Lys Ser Gly Cys Arg Phe Leu Trp Leu
149     290                 295                 300
150 Ala Arg Ile Ser Pro Glu Met Asp Leu Asn Ala Leu Leu Pro Glu Gly
151 305                 310                 315                 320
152 Phe Leu Ser Arg Thr Lys Gly Val Gly Phe Val Thr Asn Thr Trp Val
153             325                 330                 335
154 Pro Gln Lys Glu Val Leu Ser His Asp Ala Val Gly Gly Phe Val Thr
155             340                 345                 350
156 His Cys Gly Trp Ser Ser Val Leu Glu Ala Leu Ser Phe Gly Val Pro
157             355                 360                 365
158 Met Ile Gly Trp Pro Leu Tyr Ala Glu Gln Arg Ile Asn Arg Val Phe
159     370                 375                 380
160 Met Val Glu Glu Ile Lys Val Ala Leu Pro Leu Asp Glu Glu Asp Gly
161 385                 390                 395                 400
162 Phe Val Thr Ala Met Glu Leu Glu Lys Arg Val Arg Glu Leu Met Glu
163             405                 410                 415
164 Ser Val Lys Gly Lys Glu Val Lys Arg Arg Val Ala Glu Leu Lys Ile
165             420                 425                 430
166 Ser Thr Lys Ala Ala Val Ser Lys Gly Gly Ser Ser Leu Ala Ser Leu
167             435                 440                 445
168 Glu Lys Phe Ile Asn Ser Val Thr Arg
169     450                 455
281 <210> SEQ ID NO: 13
282 <211> LENGTH: 1446
283 <212> TYPE: DNA
```

E--> 284 <213> ORGANISM: ← *mandatory response*
W--> 285 <220> FEATURE:
W--> 286 <221> NAME/KEY:
287 <222> LOCATION:
288 <223> OTHER INFORMATION: pSPB264 ← *if this explains an Artificial Sequence, give source of genetic material*
W--> 289 <400> SEQUENCE: 13

```
290 atgggaaaac ttcacattgc cttatttcca gttatggctc atggtcacat gatcccaatg    60
291 ttggacatgg ccaagctctt tacctcaaga ggcatacaaa caacaatcat ttcgactctc   120
292 gccttcgctg atccgataaa caaagctcgt gattcgggcc tcgatattgg actaagcatc   180
293 ctcaaattcc caccagaagg atcaggaata ccagatcaca tggtgagcct tgatctagtt   240
294 actgaagatt ggctcccaaa gtttgttgag tcattagtct tattacaaga gccagttgag   300
295 aagcttatcg aagaactaaa gctcgactgt ctcgtttccg acatgttctt gccttggaca   360
296 gtcgattgtg cggctaagtt cggtattccg aggttggttt ccacggaac gagcaacttt   420
297 gcgttgtgtg cttcggagca aatgaagctt cacaagcctt ataagaatgt aacttctgat   480
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
298 actgagacat ttgttatacc ggatttcccg catgagctga agtttgtgag gactcaagtg  540
299 gctccgtttc agcttgcgga aacggagaat ggattctcaa agttgatgaa acagatgacg  600
300 gagtctgttg gtagaagcta cggtgttgtg gttaacagtt tttatgagct cgagtcgact  660
301 tatgtggatt attacagaga ggttttgggt agaaagtctt ggaatatagg gcctctgttg  720
302 ttatccaaca atggcaatga ggaaaaagta caaaggggaa aggaatctgc gattggcgaa  780
303 cacgaatgct ggcttggtt gaattccaag aagcagaatt cggttgttta cgtttgtttt  840
304 ggaagtatgg cgactttac tccagcgcag ttgcgcgaaa ctgcgattgg actcgaggaa  900
305 tcaggccaag agttcatttg ggtagttaaa aaggccaaaa acgaagaaga aggaaaagga  960
306 aaagaagaat ggctgccaga aaattttgag gaaagagtga agatagagg cttgatcata  1020
307 agaggatggg cgccgcaatt gttgatactc gatcatcctg cggtaggagc tttcgtgacg  1080
308 cattgtggat ggaattcgac gttggaagga atatgcgccg gtgtgcctat ggtgacttgg  1140
309 ccagttttcg cagagcagtt tttcaatgag aagtttgtga cagaggtttt ggggaccggt  1200
310 gtttcggttg ggaataagaa gtggctaagg gcagcaagtg aaggtgtgtc gagggaggca  1260
311 gtgacgaacg cggtgcagcg tgttatggtg ggagaaaatg cgtcggagat gagaaagcga  1320
312 gcgaagtatt ataaggaaat ggcgaggcgg gcggttgagg aaggcggttc gtcttataat  1380
313 ggtttgaatg agatgataga ggatttgagt gtgtaccgtg ctccagaaaa acaagactta  1440
314 aactag                                                            1446
316 <210> SEQ ID NO: 14
317 <211> LENGTH: 1488
318 <212> TYPE: DNA
```

E--> 319 <213> ORGANISM: *← response needed*
W--> 320 <220> FEATURE:
W--> 321 <221> NAME/KEY:
      322 <222> LOCATION:
      323 <223> OTHER INFORMATION: (pSPB662) *Explain source*
W--> 324 <400> SEQUENCE: 14

```
325 atggcctttc aaattcaacc agagcttcta aacttcgttt tcataccatt catggcccct   60
326 ggccactcaa tccctatgat agacttagcc aaattattcg cggaacgcgg cgtcaacgta  120
327 acgatcatcg taacacctct taacgccgca cgattcaatt ccgttattaa tcgagccgtt  180
328 gaatcaggac agtccattcg tcttctccaa gtaaaattcc ctggtgaaga agccgggttg  240
329 ccacctggat gcgaaagcgc cgagacttta ccatcttatg aattgattcc aaatttttt  300
330 accgccgtaa aaatgttaca acaaccaatc gaggaagaat tgagaaattt gatccccttta  360
331 ccaagctgcg tcatttgtga taaacacata ccctggactg ctcaaacgtg caagaatctc  420
332 cgaattccga ggataatttt cgatggaatg agctgttttg ctcctttagt aacacacgtt  480
333 ctctacgtgt ctaaggttca tgaaaccgtt cctccaaacg agccgttcgt tgttcctgat  540
334 ttccccgatg agatagagtt aacgaggttt caattgccag ggttgttgaa tccaagtcca  600
335 aggataaatt tttacgattt tcgcgaacaa gtgaagaaaa ctgaggagga ggcttatggg  660
336 gtggtggtga acagttttga ggagctggaa aaagattatt cgagatgtt tcggaaattg  720
337 aaaggggta aagtttggtg tgttgggcct ttgtcgcttt atggtaacga cgatttggac  780
338 agggctggaa gagggaataa ggcgtcgatt gatacggatc ggtgtatgaa atggcttgat  840
339 gatatgaaac agaatctgt aatttatgcc tgtttgggaa gcctgagtcg tttgtcgcgt  900
340 tcacagttcg tcgaacttgc tttgggattg gaagcatcaa acactcgtt tgttctagtt  960
341 gttaaaaccg aaggagagaa gtcgttggaa atagagaaat ggattttgga caatggattc  1020
342 gaggaaagaa cgaaagatag agggttcttg attcgtggtt ggtcgccaca agtgttgatc  1080
343 ttgtcgcatt ttgcagtggg aggattcttg acgcattgtg gttggaattc gacgcttgag  1140
344 ggcatttgtg ctggtttgcc aatggtgatg tggccgatgt cggcgaaca gttttttgaat  1200
345 gagaagttag tggtgcagat tttggggacg ggtgtgggag ttggagcgaa aagtacggta  1260
346 catttggggg atgaagagat ggatgagatg agagtgacga ggaaggggat taccaaggcg  1320
347 gtcgtggcag ttatggatag aggaactgaa gggtgtgaga ggcggagaaa ggcgaaggag  1380
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
348 cttggtgaaa tggctaagag ggcagtccaa gttgggggat cttcatgtaa gaatgtcgac   1440
349 cagctaattc aagaagttgc accattgagt gtagcgaggg atgtgtaa                 1488
351 <210> SEQ ID NO: 15
352 <211> LENGTH: 1446
353 <212> TYPE: DNA
354 <213> ORGANISM:
355 <220> FEATURE:
356 <221> NAME/KEY:
357 <222> LOCATION:
358 <223> OTHER INFORMATION: pSPB1621
359 <400> SEQUENCE: 15
360 atgggttctc tccctgaaaa tgagctcaac aaaccacatg ctgtgtgcat accctatcca     60
361 gcactagggc atttcagtcc catgctagat tttgctaagc tcctccacca aaaaggcttt    120
362 cacataacct tcgtcaacac cgagtacatc cgtctccgcc tcctcaagtc ctgtggccct    180
363 gccgccctgg acgggctacc ggactttcgc ttcatgacta tccccgatgg cctccctttg    240
364 tcggacgacg tttcgcgtga tgtcgcttcc atttctgtct ctactaacaa aacttgctta    300
365 gaacccttt  gtgaggtgct atcggacctc atggataatg gttccaaccc gccggtgagc    360
366 tgcattgtgt ccgacggggt aatgagtttc acccttgagg cggcggagag gtttggactg    420
367 ccagaggtgc tgttctggac gcccgctgct tgtggcatct tagctttcac gcagtataag    480
368 catcttgtgg agagaggata tgtacctctc aaagatacga gccaggtaac aaatggctac    540
369 ctggaaacaa tattagattg ggttccaggg atgaaggata ttcgattgag ggaattccca    600
370 actttcataa gaacgacgga cccaaacgac gttatgctgg attttctaat aaaacaagtt    660
371 gacgccaccc cgaaagccaa tgctgtgatc atcaacacgt tcgacacatt ggaaagtgac    720
372 gctctcaacg ccctctctgt catgtttccg cgcatataca cactcgggcc tctccatatg    780
373 atgttgaata tcccgaggt  cgacgaaccc tctaatgcaa tcaaatttaa tctttggaaa    840
374 gaagactcac attgcctaga ttggctcgat gtgaacgagc ccggatcagt tgtatacgtg    900
375 aattttggca gctcaacaat tctgactgtt gaacaactaa ctgaattagc atggggcctt    960
376 gctaacagca agaaaccgtt cctttggatc atcaggcctg atttagtaac tggtgcatcc   1020
377 tccatgcttc cgcctgagtt cctggtcgag actaaagaca gaagcatgtt agtgagttgg   1080
378 tgcaaccaag aacaagtgtt gaagcacccc gcgactggag tgttcttgac gcattgtgga   1140
379 tggaattcga cgattgaaag catttgcagc ggcgtgccaa tgatttgttg gccttactac   1200
380 gctgagcagc aaaccaactg taggtacagt tgtgtggaat gggaaatagg aatggagatc   1260
381 attgacaacg atgtgaagag agatgaggtg gaattgctgg tgattaagtt gatggatggt   1320
382 atcaagggaa agaaaatgaa aaagaaagct atggagtgga gaggaaagc  agaagaggcg   1380
383 gtagcttttg ggggctcttc ctacatgaat ttggataaac ttattagcga cgtgctttt   1440
384 ccataa                                                              1446
386 <210> SEQ ID NO: 16
387 <211> LENGTH: 1458
388 <212> TYPE: DNA
389 <213> ORGANISM:
390 <220> FEATURE:
391 <221> NAME/KEY:
392 <222> LOCATION:
393 <223> OTHER INFORMATION: pSPB1620
394 <400> SEQUENCE: 16
395 atggcaggtc caaattgcaa gcctcacgcc atcatgatcg cacttcctta ccaaggccac     60
396 ataactcctt ttgtcaatct tgcactaaaa cttgcttcca atggctttac aatcactttt    120
397 gttcaccttg aatttatcca ccaaatgttg tctaaagccc ataacgccac taaaactgaa    180
398 gcagatttat tttcggaagc acgagaatcc ggtctcgaca tacgttacac aacgattgac    240
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272006\J583110.raw

```
399 gatggtttcc ctttggaatt cgacagggct ctccactccg aggagtattg gcactccatg   300
400 ttgcgagatt tcccgttaca cgtcgatgag tttgttcgaa aagtcgtgga gtcagagcca   360
401 tttttagagc acttttttggt tacggatact atgtatacat ggcctgcaac cattgcaaag   420
402 aaacataatc ttgtgaatat ttcgtttttgg actgaaccag ccctggtgtt ttctttgtct   480
403 taccatataa accttctgaa gcaaaatggt cattttccat gtaaagaaaa tattgatgag   540
404 gaaataaatt acgtaccagg agttgattca ataagtacaa gggatttaat gtcttatttt   600
405 aaagaaccag gatcagaaac attagagaaa aatgttgtgc tcaaggcatt tgaaggagtg   660
406 aagaaagctg atttcatctt gcataacaca ttgcaagaac tagaatctga gacactctca   720
407 gctcttacca aaatgcagcc aaattacgcc gttggaccta ttaatttctc caaacatact   780
408 cctaaaactg tcaccaagag tctacggtct gaattcgact gcaccaactg gctcgactct   840
409 aagcctccca actctatttt atacgtctcg tttggtagtt ttattcagac aagcaaagag   900
410 gtaattgaag aaatcgctta cggtcttctc cttagtgaag ttaactttat atgggtggtt   960
411 agaacagata gtgtgagttt agaggataac gaggttttgc cggttggatt tagggatgag  1020
412 gttaaagata gggggttgat agttccgtgg tgtgatcaaa ttacggtttt gtctaatcgc  1080
413 gcggttggag gattcttgac gcattgtgga tggaactcgg tattagagag tatgtggtgt  1140
414 ggcgttccta tgatttgtta tccgttaaca tatgatcaac ctactaatag gaaactattg  1200
415 gttgatgatt ggaagattgg cattaatctt tgcgacggag cgttgattaa tagaaaagaa  1260
416 attgcagaga agattaaggc cttgatgagt gaaagtactt cagaggggtt gagggaagaa  1320
417 tctgagaaag ttaagggctt gttgaagaat gcactggaag ttggtggttc atcagagaag  1380
418 aatttcaata aatttattga ggatttgaag gcaaaaattc aaataatgaa agagcaaatg  1440
419 cctgctaata ccagttga                                                1458
421 <210> SEQ ID NO: 17
422 <211> LENGTH: 1443
423 <212> TYPE: DNA
```

E--> 424 <213> ORGANISM: *response needed*
W--> 425 <220> FEATURE:
W--> 426 <221> NAME/KEY:
427 <222> LOCATION:
428 <223> OTHER INFORMATION: pSPB1622
W--> 429 <400> SEQUENCE: 17

```
430 atgggttcca cagccgaaaa taaacagaaa acccacattg tgtgcatacc ctacccagcc    60
431 caggggcaca tcagccccat gctaaagtta gccaaactgc tacaccaaaa cggcttttac   120
432 atcacttttg tcaacacgga gtacaaccac cgccgcctca tcaagtcccg cggcccccacc   180
433 gccctcgacg gattgcccga tttccggttc gttacgatcc ccgacgggct tcctttctct   240
434 gaagccgacg ccacacagga tatcccttct ctttgtgttt caaccaccaa cacttgcttg   300
435 gagcccttttt gcgagctgct gtcgaacctc aataactccg ccccggacgt gcccccggtg   360
436 agctgcatcg tatccgatgg tgtcatgagc ttcacgttga aggcggcgga gagatttggg   420
437 ctgccggagg tgctgttctg gacgacgagt gcgtgtgggt cttggcgta tacgcagtat   480
438 aagcatctcg tggagaaagg ctatgtaccc ctcaaagata tgagccaagt aacggatgga   540
439 tatttgaaaa caagcatgga ctggattcca ggaacgaagg acatccaact aagggacttc   600
440 ccctctttca tcaggacaac agatccagaa gacatcatgc ttaatttttt aatacaagaa   660
441 actgatgttg ttccgagagc caaagctgta ataatcaaca ccttcgacat gttagaacac   720
442 gacgtcctgg aagcgctctc caccatgttt tcacgcgttt acagcatcgg ccctcttcag   780
443 ctgatgatga attatgttca caacgagtcc cttaaatcca tcagttccag tctatggaaa   840
444 gaagaaacac attgcgtcga ttggctcgat tcaaaggagc ccgaatccgt tgtgtacgta   900
445 aattttggca gcataactgt cgtgactgca gaacaactga ctgagtttgc gtgggggctc   960
446 gctaatagta agaagacttt cctatgggtt attaggcctg atatagttgc tggagactcg  1020
447 gctatgctgc cccctgaatt cgtgacgggg acaaaagata gaagcatgtt aatcagctgg  1080
448 tgtaaccaag aacaggtgtt gaatcaccca tcaattggag ggtttttgac gcacagtggt  1140
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: **US/10/583,110**   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
449 tggaattcga cgattgaaag tatagtcgag ggagttcctg tgatttgctg gcctttcttt   1200
450 gctgagcagc aaacaaattg taggttcagt tgcgtggaat gggaaatagg aatggagatt   1260
451 gataataatg tgaagagaga tgaggttgaa gttttggtga gggaattgat ggatggagag   1320
452 aggggaaga aaatgaagga gaaagctatg gagtggaaag ggaaagcatt agaggcaact   1380
453 gcacttgggg gctcttccta cttgaacttg gaaaaactaa ttaaggaggt gcttttgcat   1440
454 taa                                                                 1443
456 <210> SEQ ID NO: 18
457 <211> LENGTH: 1407
458 <212> TYPE: DNA
```

E--> 459 <213> ORGANISM: *response needed*
W--> 460 <220> FEATURE:
W--> 461 <221> NAME/KEY:

```
462 <222> LOCATION:
463 <223> OTHER INFORMATION: pSPB1610
```

W--> 464 <400> SEQUENCE: 18

```
465 atggcatctt ctccccataa ccagccaacc acgccccgcc acgtggtggc cctaccctac    60
466 cccggccgcg gccacataaa ccccatgctc aacatctgca aagccgtagc ggagaagagc   120
467 agccacatca acataacaat catcctaacc gaggaatggc tcggcttaat cggctcagcc   180
468 gacaagccgc cgaacataag ctacgccgcg ataccgaaca ttctgccgtc ggagcacgtt   240
469 cgcggcgagg atccacatgg tttttgggcg ctgtttggc agaagatgga ggagccggtt   300
470 gatcggctgc tggacgagct tcggcttaat aataacaagc cggagtttgt gatagccgat   360
471 gctttcttgc attgggcggc tgacgtggcg ggcaggagga atattccctt ggcatctgtt   420
472 tggccaatgt cggcgtccac gttcacggtg ctttaccact ttgaccttct cgttgaccac   480
473 ggacactttc cgatcgacat accagtgaat ggagatgcta ttgtggatta catcccggga   540
474 ctccctccag ttcgcgtcgc agatttttcca aaagacataa gaaaacaaga agacgcatcc   600
475 ttcgtcctta aactcattcc caactcacca aaattcatca tcttcacttc aatttacgac   660
476 ctcgaatcca agatcatcga cgctctaaag caaaaatctt ccttctcaat ctacaacatt   720
477 ggtcctcatg cttcctattc caaactcaaa cacatcctca actcggataa aatcacgaaa   780
478 cctgatcaag ataaccccga ctacttaaaa tggttagatc tccaacctcc caactccgtc   840
479 ttgtacattt cactcggcag tttcctatcc atttcgcag cccaaatgga tgaactcgca   900
480 accggaatac gaaactctgg tgtccgcttt ttgtgggtgg cacgtggcga aacaaaccgg   960
481 ttgaaagaga tttgttgtga tcatgaaaag gggctgatca tagaatggtg cgatcaaatg   1020
482 caggttcttt ctcattcttc ggttggtgga ttcttgtcgc attgtggttg gaattcgact   1080
483 aaagaggcgt tgatggccgg ggtgccgttt ttgactattc caattatgtt tgatcaagtg   1140
484 tctaacgcga aggcggtcgt ggaagattgg agggtggggt ggagggtggt gaatgagttt   1200
485 aatgaagaag agttggtggg aggagatgag attgcgaata ttgtgaggag gtttatggat   1260
486 atggaaaatg gtgagaggaa agagttgacg aaaaatgtga aagaggtgca gaagatttgt   1320
487 gcgagagagt tcgaagatgg agatggacag tcgtttgagt ttaatgttga agtttggtt   1380
488 caattgattc tgcaattggg tccgtaa                                        1407
490 <210> SEQ ID NO: 19
491 <211> LENGTH: 1428
492 <212> TYPE: DNA
```

E--> 493 <213> ORGANISM: *response needed*
W--> 494 <220> FEATURE:
W--> 495 <221> NAME/KEY:

```
496 <222> LOCATION:
497 <223> OTHER INFORMATION: pSPB1609
```

W--> 498 <400> SEQUENCE: 19

```
499 atgaacaaca caacccaaca acaaacagta gcattagcac tagcacctca ctgtttaatc    60
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

          Input Set : A:\PTO.RJ.txt
          Output Set: N:\CRF4\06272006\J583110.raw

```
500 gtcccattcc cattccaagg ccacattaac cccttactcc aattcgccaa acgcctcata   120
501 actcaccaca acaaaaacct ccaaatcaca ttcgcactca ccaaattcat cctcaccaac   180
502 ctctcctccg gtgccggaga atcatccttc tctctccggt caatctccga cggcttcgac   240
503 gccggcggcc gcgctcaggc caactccggc gccgaatacc tctccaaatt ccgcgagatc   300
504 ggatctcaaa ccctaaccga acttatccaa gacctatccg aatcgggtcg acccgttgac   360
505 tgcgtggtct acgacccgtt cgtaccttgg gccttagatg ttgccaaggg taaattcgga   420
506 atttcaacgg cggcgttttt tacgcagtcg tgtgcggtgg ataatatata cagtcgggtt   480
507 tataacggcg atttggagct gccgttgccg gagaatgagg tggttagggt tccgggtttg   540
508 ccggagatgg agccgtttga gatgccgagc tttgtgtatt taaacgggtc gtacccgtcg   600
509 agttttgaga tggttgtggg tcagtttagg aatgttgatg aggcggattg ggtttttgtc   660
510 aacactttt atgagttgga gaaagaggtc attgactgga tgtcaaaatc ttggcgagtg   720
511 aaagcaattg gacctaccat accatcaatg ttcatggaca agagattgca agaggacaaa   780
512 tcatacggtc ttagcatgtt caagcataca acaaatgact gcataaattg gctcaacgga   840
513 aaacaatcaa aatccgtcat ttatgtcgca tttggaagtc ttgcagaatt atcccacgac   900
514 caaactcaag aactggcaca cgccttaaca acctacgaca aacacttctt atgggttgta   960
515 cgatcatcgg aagaagctaa gcttccccaa aattttgcta acgaaacatc taagaaaggg  1020
516 ttgatagtgt cgtggtgccc tcaattagag gtcttgtcgc acgaggccat cggttgtttc  1080
517 gtgactcatt gtggttggaa ttcaacgctc gagggattga gtttgggggt gcctatggtg  1140
518 gcgatgccac agtggacgga tcagagtacg aacgctaagt ttatcgtgga tgtttggggt  1200
519 gtgggtgttc gggctaaggt ggacgagggg ggattagcga ggcaagatga gatagttcgt  1260
520 tgcttaggga gcgtcatgga aggggagaac ggagaaaaga taagaaagaa tgcgaatgaa  1320
521 tggaaggaac gggcgtgcaa tgcagttgat gaaggggggga gttcagacaa aaatattgaa  1380
522 gaatttgtta ctacgttgat aagttcccat gacttgcgtc aagagtaa              1428
524 <210> SEQ ID NO: 20
525 <211> LENGTH: 1425
526 <212> TYPE: DNA
```
E--> 527 <213> ORGANISM: ←response needed
W--> 528 <220> FEATURE:
W--> 529 <221> NAME/KEY:
     530 <222> LOCATION:
     531 <223> OTHER INFORMATION: (pSPB1617)
W--> 532 <400> SEQUENCE: 20
```
533 atgtctagtg agagccaaat aaacttagtg ttcatccctc tccctgtaaa gggacacatt    60
534 gtctcaacgc tagagacggc aaagctactc gtcgatcgaa acaaacgcct caccatcaca   120
535 atcctcctca tgaagctgcc agtcgacgcc aaggtagatg attccttcac aaaaaatccc   180
536 tcctgctctc aaataacttt tgtacatctc cctcgaatcg agcacagttc catggaacca   240
537 ccgggaactc ccgaatcctt tgtacacagg ttcgtcgaga gccaaaaatg tctcgtaaga   300
538 gatgcggtgg ttaaagcaac ggagggctca aaatcaaaca ggctagccgg atttgtaatc   360
539 gacatgttct gcaccccgat gattgatgtg gccaatgaat ttggcgtccc gacatacgtg   420
540 gctttcacgt ccggggccgc aactctcggg ctattgttcc atttgcagag tcttagagat   480
541 gaatttaatc aggacgtgaa ggagtacgag aactcggaag ttgagatatc gatcccggct   540
542 tatgttaacc cgttcccttc caaatccttg ccgtctcctg tcttcaacga ggacggtgtt   600
543 tttcttagtc ttgcaaaggg gttcagagag gctaaggta tattgatcaa cacctttta   660
544 gaatttgaat cccatgccat taaatcgctc tccaacgatg cgagaatccc gcctgtttac   720
545 cccatcgggc cagtaattca cgccacggaa gataatgcaa acaaaggaaa gcaggacgaa   780
546 atcatcgcgt ggcttgacga gcaacctgat tcatccgtcg tgtttctttg cttcggaagc   840
547 gctggatgct ttgaagaaaa tcaagtgaag gagattgcag tggcgctcga caaaagtgga   900
548 taccggtttt tatggtcatt gagaaagccg cctcccaaag aaaaagcgga gtttccaggg   960
549 gagtacaaag attttaatga agttttacca gaagggttct acaacgtac gtccgggaga  1020
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: **US/10/583,110**   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
        550 ggtaaggtaa taggatgggc tccgcagatg gccgtgttgt ctcacaatgc ggtgggagga   1080
        551 ttcgtgtcgc attgcggctg gaactcgacg ttggagagtg tttggtgcgg agtgccaatg   1140
        552 gccgtgtggc cattggcggc cgagcaacat gcgaacgcgt tccagttggt gaaggagttg   1200
        553 ggaattgcgg tggagattaa gatggattat aggaagaaca gtggtgtgat tgtggaggca   1260
        554 aaaatgattg agaaaggaat cagggagttg atggacccgg aaaatgagat aaggggtaat   1320
W-->    555 gtgaaagtga tgaaaaagga gagtaggana gctgtcgtgg atggtgggac ttcttttgat   1380
        556 tacttggatc gttttgttga aactgtcgtg aataatgttt tgtga                    1425
        558 <210> SEQ ID NO: 21
        559 <211> LENGTH: 1446
        560 <212> TYPE: DNA
E-->    561 <213> ORGANISM:
W-->    562 <220> FEATURE:
W-->    563 <221> NAME/KEY:
        564 <222> LOCATION:
        565 <223> OTHER INFORMATION: pSPB1615
W-->    566 <400> SEQUENCE: 21
        567 atgggttccg tagccggaaa cagttacaaa cggcctcatg ctgtgtgcat accccttcccg    60
        568 gcgcagggg acatcaaccc catgctgaag ttggccaaac tcctccacca aaagggcttc    120
        569 cacatcacat tcgtcaacac agagtacaac caccgccgct tgctcaagtc cctcggcccc    180
        570 gacgctctcg atggcttgcc ggatttccga ttcgcaacca tccccgacgg tcttcctccg    240
        571 tctgacgcgg acgtcactca ggatgttcct tctctttgta tgtccaccac taacacttgc    300
        572 ttggagccct ttaccgagtt gctgttgaaa ctcaataact ccggcccgga cgtgccaccg    360
        573 gtgacctgca tcgtctcgga tggtgtcatg agcttcacat tgaaggcggc ggagaggttt    420
        574 gcgctgccgg aagtgctgtt ctggacgacg agtgcgtgtg gtttcttggc gtacacgcag    480
        575 tataagcgtc tcttggagaa aggctatgtc cctctcaaag atatgagcca gttaacaaat    540
        576 agctatctgg aaacaaccct cgactgggtt ccaggaatga aggatatccg attaagggac    600
        577 ttcccatcat tcatcaggac aacggatcca aaagacatca tgtacaattt cgtattacaa    660
        578 gaaaccgacg ctgtctccag agccaaagct ctgatcatca acacctttca tacattggaa    720
        579 cacgacgttg taaatgccct ctccaccatg tttccacgtg tttacaccat cggctctctt    780
        580 cagctgatgt tggaccaagt tcatgacaag agccttaacg ccatcaactc caatctctgg    840
        581 aaagaagaat cgcaatgcat cgattggctc aattcaaaag agcccgaatc cgttgtgtat    900
        582 gtgaatttcg gtagtgtcac tgttgtgact gctcaacaac tgacggaatt gcgtggggg    960
        583 cttgcgaaca gcaacaagac ttttttatgg gttattaggc ctgatatagt tgttggagac   1020
        584 tcggcaatgc tgccccctga attcttgacg gacacggaag acagaagcat gctaataagc   1080
        585 tggtgtaacc aagaacaggt gttgaggcac ccttccatcc gaggattttt gacgcacagt   1140
        586 ggttggaact cgacgcttga aagtattgtc agcggagtgc ctatgatatg ttggcctttc   1200
        587 tttgctgagc aacagacaaa ttgtaggttc agttgcgtgg aatgggaaat aggaatggag   1260
        588 attgacaata atgtgaagag agatgaggtt gaggtgctgg tgagagagtt gatggatggt   1320
        589 gaaaagggga agaaatgaa gaagaaagct atggagtgga agatgaaagc agaagcagca   1380
        590 gctgcccctg ggggaccttc gtctttaaat ttggaaaaac ttattgagga ggtgcttttg   1440
        591 caataa                                                                1446
        593 <210> SEQ ID NO: 22
        594 <211> LENGTH: 1308
        595 <212> TYPE: DNA
E-->    596 <213> ORGANISM:
W-->    597 <220> FEATURE:
W-->    598 <221> NAME/KEY:
        599 <222> LOCATION:
        600 <223> OTHER INFORMATION: pSPB660
```

needs exploration (see item 9 on Error Summary Sheet)

← response needed

← response needed

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: **US/10/583,110**   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
W--> 601  <400> SEQUENCE: 22
     602  atgaaggctc atgcagtgat gcttccttgc cccgtacaag ggcacttaaa tcctatgctg      60
     603  aaactggcca aaatattgca ttcaagaggc ttcttcatca cattcgtgaa cacggaattc     120
     604  aatcacaatc gtctagtgcg tgcgagaggc cccgaatctg ttaaaggtcg cgatgatttt     180
     605  cagttcaaaa ccatacctga tggactaccg ccttttgata aggacgcaac gcaagacata     240
     606  cctcaactgt gtgattctct tcaaaagaat ggtcttcctc cattgttgga cctcattaaa     300
     607  agtattaatg attcaccgga ctgtccaaat gttacctgta tagtgattga tttggccatg     360
     608  agtttcgctc ttgatgcggc cgaggtgttc aaaattccca cggtgtactt ttcgccaact     420
     609  agtgcttgtg gattcatggg gtttttgcaat tatgaagagc ttgtgaatcg aggattgttt     480
     610  ccacttaaag atgaaagtca aataactaat ggctatcttg ataccaaact agactgggtg     540
     611  ccagggatga agaacattag gctcagagat tttcctagtt tcatccgaac gactgatcca     600
     612  gatgatatca tggtgaactt catgattttt aacatgaaga atgcgcctcg tgcaaaggct     660
     613  gtggtagtca acacattcga tgaattggag aaagatgtat tggaggccct aagtaaaaaa     720
     614  tttgatcatg ttttttccat aggcccactc caattgatgg agaaggcttt ccaaaagcct     780
     615  gaggtaaaat ctataggatc aagcttgtgg aaagaagaca acacgtgcat cgcctggctc     840
     616  aacggcaggg agccaaattc tgtgttgtac gtgaactttg gaagcatcac agtgttgtca     900
     617  cctcaacaac tattggagtt cgcatggggc ctagccaata gcaaccatta cttttttgtgg     960
     618  atcataaggc cagatttggt aagtggagaa tctgcgattt tatccgaaga gtactcaaag    1020
     619  gaagttgaag ggcgggcgat gatggtgcgt tggtgctctc aagagcaagt attggcccat    1080
     620  ccttcggtag gtggattctt gacacattct ggctggaact cgactatcga aggaatgtca    1140
     621  gaaggtgttc ctatgatttg ttggcctttt tttgctgacc aacagaccaa ttgtcggtat    1200
     622  gcatgcacgg agtgggagat tggaatggag attgaaggag aggttacgag ggataaagtg    1260
     623  gcggatttgg tgaaaatatt gatggaggag ggaaggggag agcgatga                 1308
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     626  <211> LENGTH: 1506
     627  <212> TYPE: DNA
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W--> 629  <220> FEATURE:
W--> 630  <221> NAME/KEY:
     631  <222> LOCATION:
     632  <223> OTHER INFORMATION: pSPB658
W--> 633  <400> SEQUENCE: 23
     634  atggccattc atgaacaaaa acctcacttt gtcctgttcc ctttcatggc acaaggccat      60
     635  atgattccca tggtagatat cgccagatta ctcgcgaagc gcggtgtcac aatcaccatt     120
     636  ctactcacac cccacaatgc caacagggtc aaaacagtca ttgctcgtgc aatcgattca     180
     637  ggactaaata tcaatgtcat ccacttcaaa tttccatccg ttgaggtcgg attgcccgaa     240
     638  ggttgtgaga atttcgatat gctccctgac atcaatggcg cattgcagtt tttcaaagcc     300
     639  actttcatgt tacaagaaca ggtcgaagag ttgcttccaa agctcgagcc tcttccgagc     360
     640  tgcctaattg ctgatatgtg ctttccatgg acaacaaatc ttgctttgaa gttaaatgtt     420
     641  ccaagaattg tgtttcacgg acaagttgc ttttctctcc tatgtatgca cgttttagga     480
     642  acttctaagg atttcgaagg tgtgactaac gaaacggagt acttccttgt gcctggatta     540
     643  ccagataaaa tcgaaataac caaaattcag cttaggggca cccttattca aatgaattca     600
     644  gactggacga gtttcgtga tgaggtgcga gaggctgagg taaaagcatt ggaacggtg      660
     645  gccaatactt ttgaagattt ggaaccagag tatgtcaaag aatacagcag agttaaaggc     720
     646  aaaaaagtct ggtgcatagg tcctgtttca ttatgcaaca agatggcat agacaaggcc      780
     647  gaaagaggta acatggcttc aatcgacgca caccattgct tgaagtggct caattcacac     840
     648  gaacaaaagt ctgttatttta cgtctgcctt ggaagcatat ctcgcctcgc tacttcacaa     900
     649  ctgatagagc ttggattggc tttagaagca tcaaacagac cttttatttg ggtagttaga     960
     650  gatccatcac aagaacttaa aaaatggttt ttgaatgaga aatttgagga aagggtaaag    1020
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(handwritten annotations present: "←response needed→ (same errors in Seqr 28-31, 34, 41" and a circle around "pSPB658" with an arrow pointing to it)

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